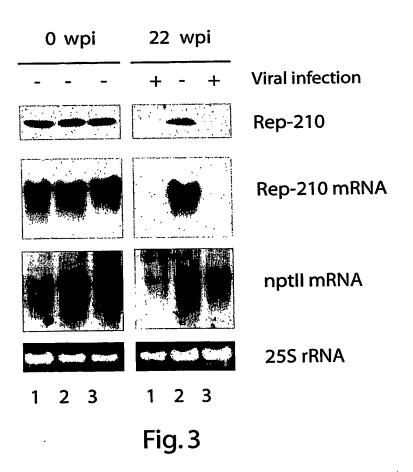


Fig. 1

0 wpi	4 wpi	8 wpi
NI NI	++-+- NI NI	NI NI Viral infection
		Rep-210
1 2 3 4 5 6 7	1 2 3 4 5 6 7	6 7

Fig. 2



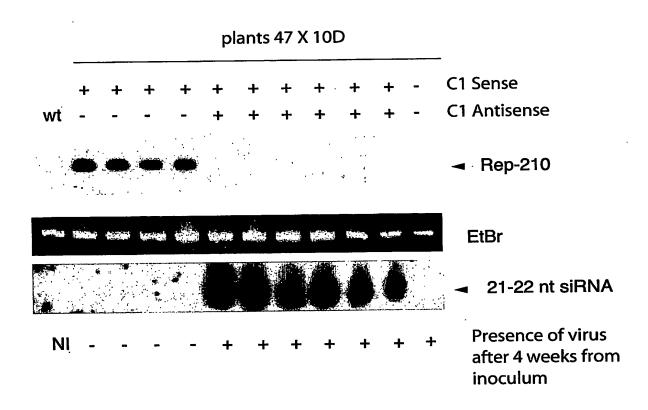


Fig. 4

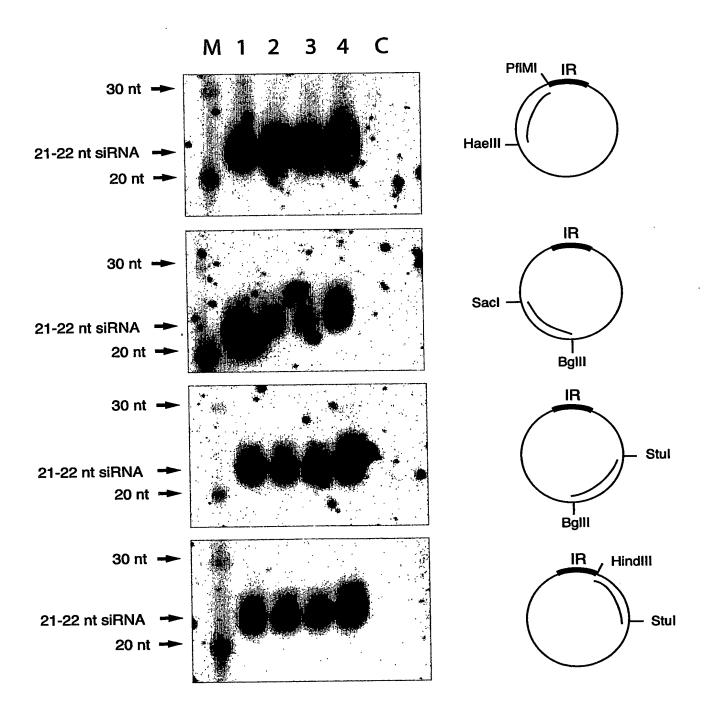


Fig. 5

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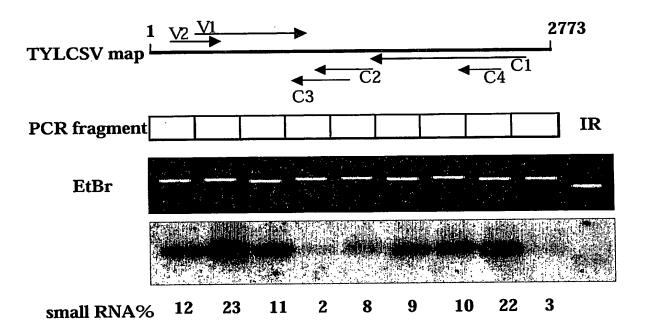


Fig. 6

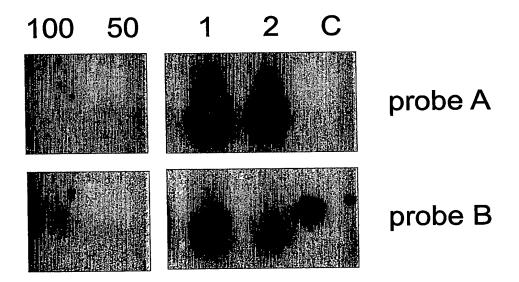


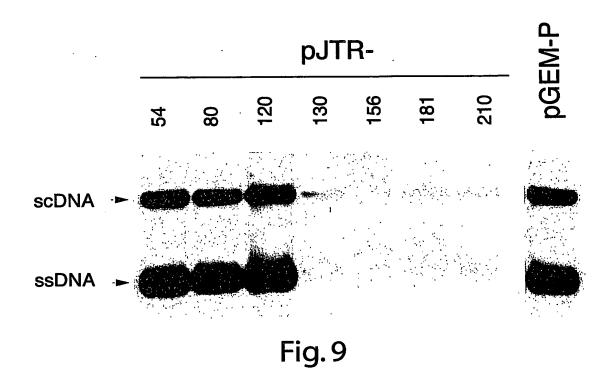
Fig. 7

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## SEQ ID No 8

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gacagcaaaaatgccaagatcaggtcgttttagtatcaag 80
gctaaaaattatttccttacatatcccaaatgtgatttaa 120
caaaagaaaatgcactttcccaaataacaaacctacaaac 160
acccacaaacaaattattcatcaaaatttgcagagaacta 200
catgaaaatggggaacctcatctccatattttgatcaat 240
tcgaaggaaaatacaattgtaccaatcaacgattcttcga 280
cctggtatccccaaccaggtcagcacatttccatccgaac 320
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tGAATTC 447



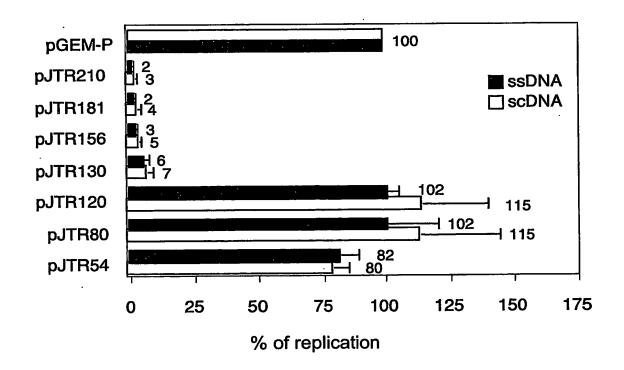


Fig. 10

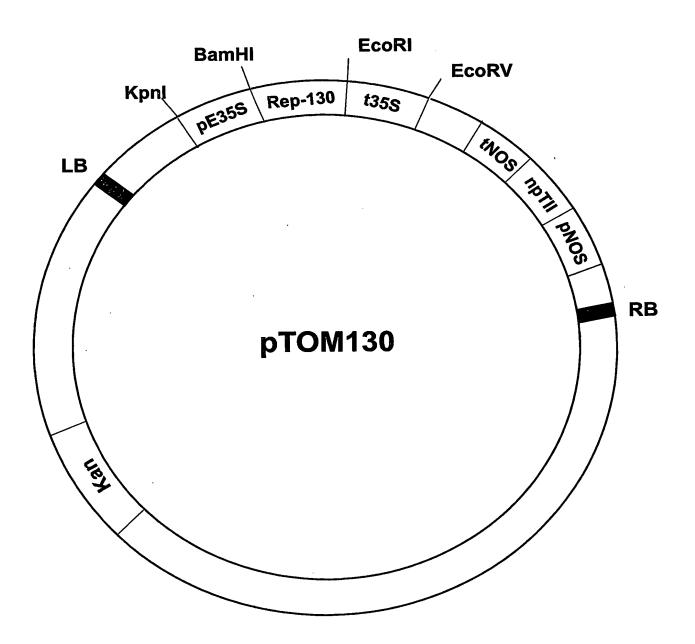


Fig. 11

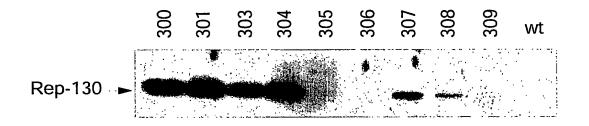


Fig. 12

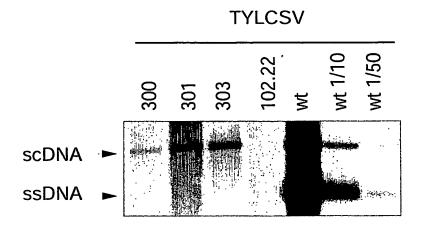


Fig. 13

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303 WT 402 403 406411 413 416 417

Rep-130

Fig. 14

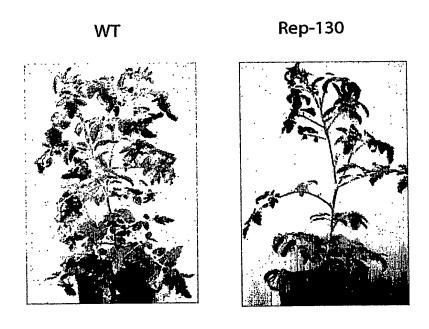


Fig. 15

12/16											
(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) Infinus (SEQ ID No 2)	(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) _minus (SEQ ID No 2)	(SEQ ID No 1) _minus (SEQ ID No 2)	(SEQ ID No 1) _minus (SEQ ID No 2)	(SEQ ID No 1) _minus (SEQ ID No 2)	(SEQ ID No 1) minus (SEQ ID No 2)	(SEQ ID No 1) _minus (SEQ ID No 2)
Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silending_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silending_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQID No 1) _Seq_cod_Rep210_sllencing_minus (SEQID No 2)	Seq_cod_Rep210_wild_type (SEQ.ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ.ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQID No 1) _Seq_cod_Rep210_sllanchig_minus (SEQID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)	Seq_cod_Rep210_wild_type (SEQ ID No 1) _Seq_cod_Rep210_silencing_minus (SEQ ID No 2)
10 40 40 40 40 40 40 40 40 40 40 40 40 40	io i	120 120 120 130 140 140 150 150 160 150 150 150 150 150 150 160 150 150 150 150 150 150 150 150 150 15	1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0 1/0	240 240 240 240 240 240 240 240 240 240	2go 3go 3go 3go 3go 3go 3go 3go 3go 3go 3	340 340 340 340 340 340 340 340 340 340	390 420 440 410 420 420 430 440 386 C A A C G C A G G C A G G C T T A C G C A A T T A A C G C A G G C T C T A C G C A G G C T C T A C G C T A A G G C T A G G C T A A G G C T A	450 440 440 450 450 470 460 TEAR ATTAGETT CATATATATATA TA CONTINUE AND A TO A CONTINUE AND A TO A CONTINUE AND	spo	ssi TTTTATCTTCTTCGATCAAGTTCCTGAACTTGAACTTGAACTGGGTTTCCGA Ssi TITTATCTTCTTCGATCAAGTTCCTGAACTTGAACTTGAACTGGGTTTCCGA Ssi TIGGTTAAAGTTCTTCGAATCAAGGGTTCCGAA	606 EAJA A C G T FT A T G G A T G C C G C G G G G G G G G G G G G G G
	8 8	==	衰衰	ឆ្គីឆ្គ	276	88	ਲਲ	22	44	යා යා	9 9

Fig. 16A

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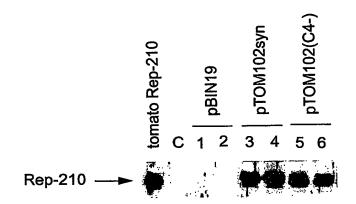


Fig. 17

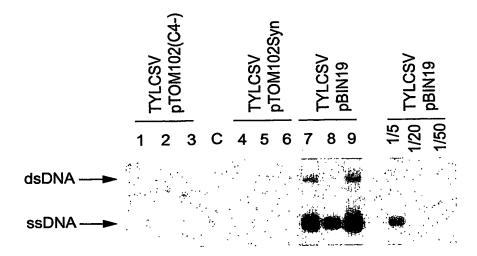


Fig. 18

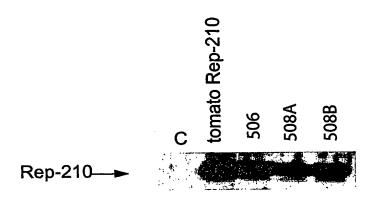


Fig. 19

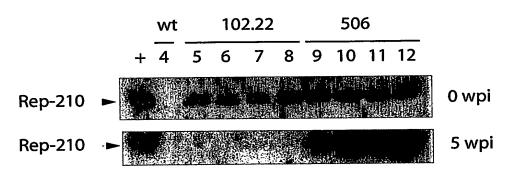
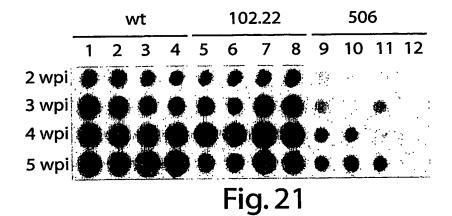


Fig. 20



16/16									
TYLCSV CP (SEQ ID No 12) TYLCSV CP silencing minus (SEQ ID No 6)	0 TYLCSV CP (SEQ ID No 12) TYLCSV CP silencing minus (SEQ ID No 6)	0 TYLCSV CP (SEQ ID No 12) TYLCSV CP Silencing minus (SEQ ID No 6)	TYLCSV CP (SEQ ID No 12)	0 TYLCSV CP (SEQ ID No 12) TYLCSV CP silencing minus (SEQ ID No 6)	TYLCSV CP (SEQ ID No 12) TYLCSV CP silencing minus (SEQ ID No 6)	L T TILCSV CP (SEQ ID No 12) T TILCSV CP silencing minus (SEQ ID No 6)	TYLCSV CP (SEQ ID No 12)	720 : A TYLCSV CP (SEQ ID No 12) : A TYLCSV CP silencing minus (SEQ ID No 6)	TYLCSV CP (SEQ ID No 12) TYLCSV CP silencing minus (SEQ ID No 6)
70 80 CTGAACTTCGACAGCCCGTA	O 150 160 160 160 160 160 160 160 160 160 16	S C A G	340 340 340 340 340 340 340 340 340 340	0 ABABACABATCATACTAACC GAAACAGAATCAGACTAATC	460 470 470 480 TITGGTCAAGTTTTAACATGTTTTTTTTTTTTTTTTTTTT	SSO AGGAAGTTTCATGCTACGG AGBAAGTTCCATGCBACGG	O 630 640 A 1 A 1 A 1 A 1 A 1 A 1 A 1 A 1 C C A 1 G 1 G 1 G 1 A 1 A 1 A 1 A 1 A 1 A 1	710 GTACTCATGCTTCTAACCC GTACGCAGCATCTAATCC	
40 50 50 60 60 COTCGAAGA GTCTGTCTTGTCGTAGGAAGA	120 140 140 140 140 140 140 140 140 140 14	210 ITGTGAAGGTCCCTGTAAI	290 AACTAGGGGTTCTGG GACTAGAGGTTCAGG	370 380 37 TGGATGGATGAAAACATAAAAAAAAAAA TGGATGGAGGAATATCAAGAA	450 1 A C T A G T C C T A T G G A T 1 A C G A G G C C B A T G G A G	530 TAGGTATCAAGTAAT TAGATATCA <mark>G</mark> GT <b>G</b> AT	610 620 AAGAGATTTTTTAAAATTACCC AAAAGATTGTTTAAGATGAAGACTC	690 FGTTATTGTATATGG FGTTETTATAGATGG	TTO TTO CTGTAACAAATTAA CTGTGACAAAGTAG
30 TACTAATTCAACGCCC	110 ACTGTCCAAGGCATCA	190 CCCTGATGTACCTCCGC CCCMGATGTGCCTCCM	270 280 FIGUGCGTGTGTTAGTGATGT FIGTTCGTTGGGTTTGTGTGT	350 350 360 TATATAGAAAGATTT	430 AGACCGAAGGC AGAICGAAGI	Sio S20 ACGGTGAAGAACGACTTACGGGA ACGGTGAAAAGGAMTTGCGNGA	Syo 600 GAAGGAGCAGTGTTTGCTGAAGAGAT GAANGGAGCANTTGTTAGTGAAAAAAT	610 680 AAAATCATACTGAGAATGCCT	750 750 760 CGIATTTATGATGCCCGIATTTTTTTTTTTTTTTTTTTTT
10 20 A T G C C G A A C C G G C G A T A A T G C C B A G B G A A C F G G F G A T A	TACCAGCCGTGCTGCTGCCCCC	AATGTACAG BATGTATCG	250 260 GATGACGTCAAGCATACCGGTG GALGGALGTGAAGCACGGBG	340 ACGTTTTGTATCAAGTCAATT GCGTTTGTGTATTAAGTCTATT	410 420 AAGTGTTTTCCTTGTTCGAGGGTTCTTTTTTTTTTTTTT	490 500 GATAATGAACCCAGTACTGCTA	Syo Syourge Syour Control Syour Control Syour Control Syour Control Syour Control Synthesis Synt	650 660 ACCAAGAGCAGGCGAAGTATG ACCAGGAGCAAATATG	730 740 GTGTACGCTACGTTGAAATA GTTTACGCAACGTTAAGATG
1 144	# # # # # # # # # # # # # # # # # # #	161	241 (	321	401	481	561	641	721

Fig. 22